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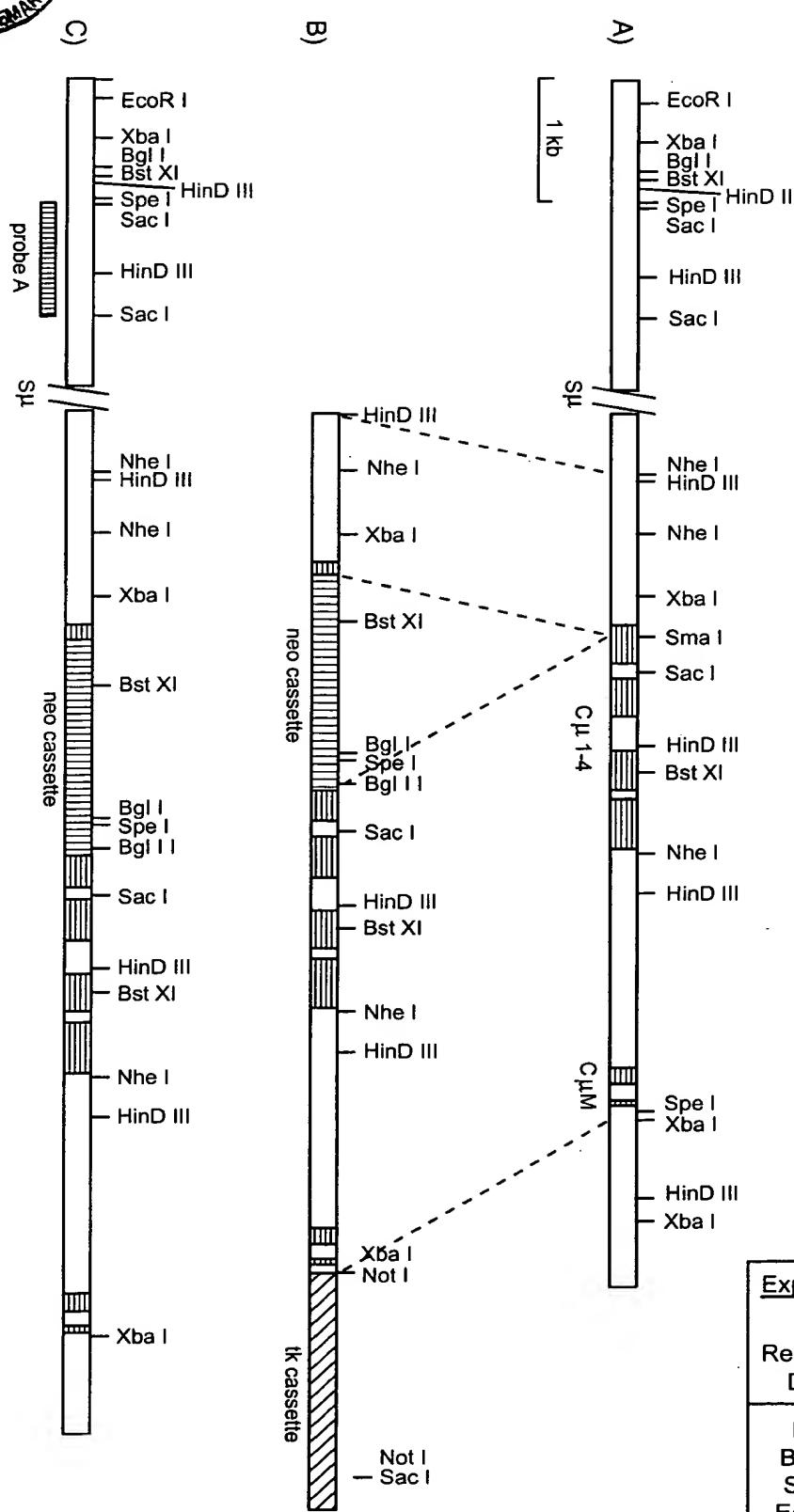
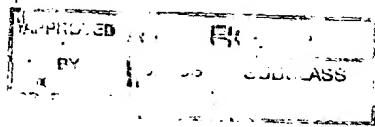


FIG. 1

Expected Fragment Sizes (kb) using Probe A		
Restriction Digest	wild type	mutant
Bgl I	15.7	7.7
Bst XI	7.3	6.6
Spe I	9.9	7.6
Eco RI	12.5	14.3



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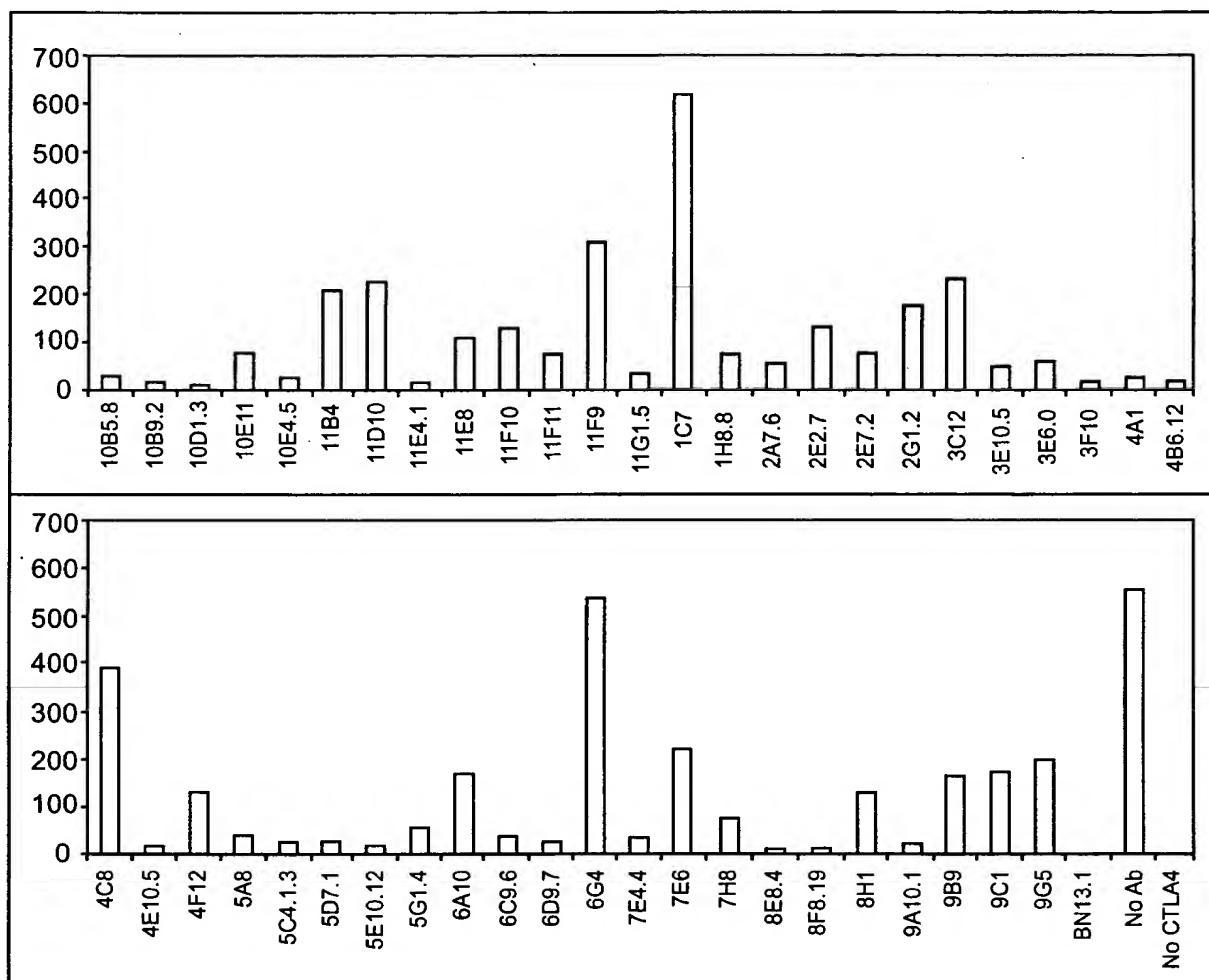


FIG. 2

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CLASS
SUBCLASS



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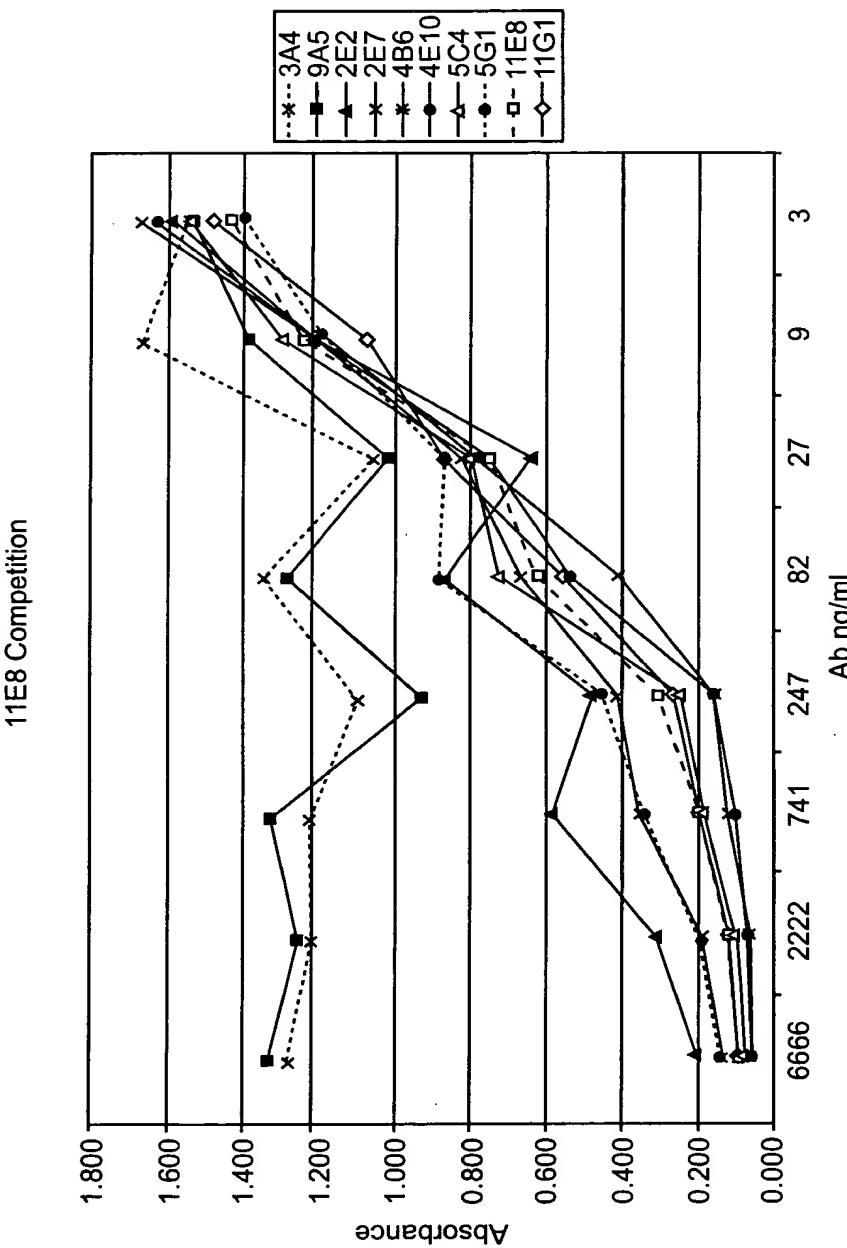
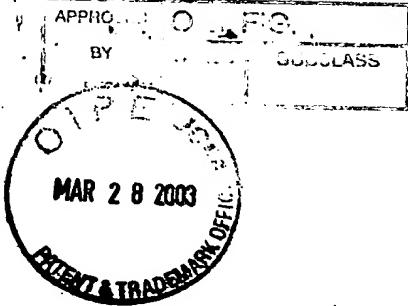


FIG. 3



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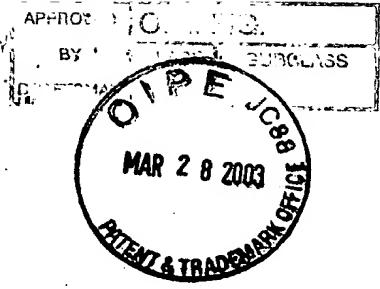
10D1.3 VH (SEQ ID NO:2)

TGGGGGAGGC	GTGGTCCAGC	CTGGGAGGTC	CCTGAGACTC	TCCTGTGCAG	50
CCTCTGGATT	CACCTTCAGT	AGCTATACTA	TGCACTGGGT	CCGCCAGGCT	100
CCAGGCAAGG	GGCTGGAGTG	GGTGACATT	ATATCATATG	ATGGAAACAA	150
TAAATACTAC	GCAGACTCCG	TGAAGGGCCG	ATTCAACCATC	TCCAGAGACA	200
ATTCCAAGAA	CACGCTGTAT	CTGCAAATGA	ACAGCCTGAG	AGCTGAGGAC	250
ACGGCTATAT	ATTACTGTGC	GAGGACCGGC	TGGCTGGGGC	CCTTGACTA	300
CTGGGGCCAG	GGAACCCTGG	TCACCGTCTC	CTCAGCCTCC	ACCAAGGGC	349

10D1.3 VK (SEQ ID NO:3)

CTCCAGGCAC	CCTGTCTTG	TCTCCAGGGG	AAAGAGCCAC	CCTCTCCTGC	50
AGGGCCAGTC	AGAGTGTGG	CAGCAGCTAC	TTAGCCTGGT	ACCAGCAGAA	100
ACCTGGCCAG	GCTCCCAGGC	TCCTCATCTA	TGGTGCATT	AGCAGGGCCA	150
CTGGCATCCC	AGACAGGTT	AGTGGCAGTG	GGTCTGGGAC	AGACTTCACT	200
CTCACCATCA	GCAGACTGGA	GCCTGAAGAT	TTTGCAGTGT	ATTACTGTCA	250
GCAGTATGGT	AGCTCACCGT	GGACGTTCGG	CCAAGGGACC	AAGGTGGAAA	300
TCAAACGAAC	TGTGGCTGCA	C			321

FIG. 4



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SEQ ID NOS: 4, 6 & 8 (respectively)

VKA-27
Germline: GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTC GAG CCT TCT TGG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC
10D1: -----
4B6: -----
CDR1
VKA-27: AGG GCC AGT CAG AGT GTT AGC AGC TAC TTA GCC TGG TAC CAG AAA CCT GGC CAG GCT CCC AGG
10D1: -----
4B6: -----
-T- -----
CDR2

VKA-27: CTC CTC ATC TAT GGT GCA TCC AGC AGC ACT GGC ATC CCA GAC AGG TTC AGT GGC AGT GGG TCT GGG
10D1: -----
4B6: -----
-T- -----
CDR3 J_{k1}

VKA-27: ACA GAC TTC ACT CTC ACC ATC AGC AGA CTG GAG CCT GAA GAT TTT GCA GTG TAT TAC TGT
10D1: -----
4B6: -----
-T- -----
CDR3 J_{k1}

VKA-27: CAG CAG TAT GGT AGC TCA CC -----
10D1: -----
4B6: -----
-G TGG AGC TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C/

SEQ ID NOS: 10 & 12 (respectively)

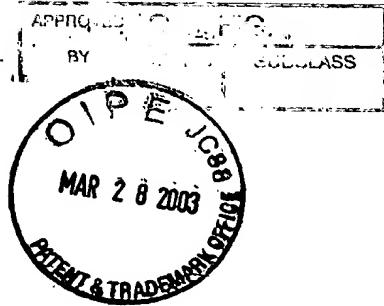
VKL-15
Germline: GAC ATC CAG ATG ACC CAG TCT CCA TCC TCA CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGT
1E2: -----
CDR1

VKL-15: CGG GCG AGT CAG GGT ATT AGC AGC TGG TTA GCC TGG TAT CAG AAA CCA GAG AAA GCC CCT AAG TCC
1E2: -----
CDR2

VKL-15: CTG ATC TAT GCT GCA TCC AGT TGG CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA TCT GGG ACA
1E2: -----

FIG. 5

1 of 2



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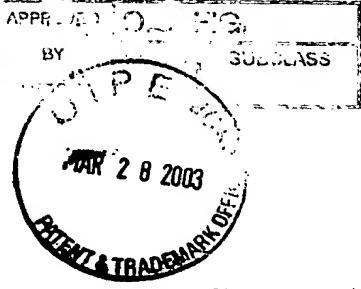
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CDR3-

VK L-15: GAT TTC ACT CTC ACC ATC AGC CTG CAG CCT GAA GAT TTT GCA ACT TAT TAC TGC CAA CAG TAT AAT
1E2: ---

VK L-15: AGT TAC CCT CC J_{k1}
1E2: --- --- --- --G ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C/

FIG. 5
2 of 2



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SEQ ID NOS: 14, 16&18 (respectively)

VH 3-30.3
Germline: CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG TCC CTG AGA CTC TCC TGT GCA GGC
10D1: -----
4B6: -----

VH 3-30.3: TCT GGA TTC ACC TTC AGT AGC TAT GCT ATG CAC TGG GTG CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
10D1: -----
4B6: -----

VH 3-30.3: GCA GTT ATA TCA TAT GAT GGA AGC AAT AAA TAC TAC GCA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC AGA
10D1: A-- T-- -----
4B6: A-- T-- -----

CDR2

VH 3-30.3: GAC AAT TCC AAG AAC ACG CTG TAT CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT
10D1: -----
4B6: -----

CDR3

VH 3-30.3: GCG AGA
10D1: --G ACC GGC TGG CTG GGG CCC TTT GAC TAC TGG GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA G/
4B6: --G -----

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SEQ ID NOS: 20&22 (respectively)

VH 3-33
Germline: CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG TCC CTG AGA CTC TCC TGT GCA GGC
1E2: -----

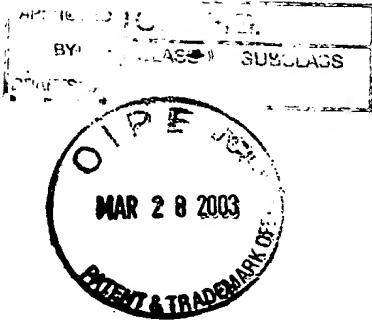
VH 3-33: TCT GGA TTC ACC TTC AGT AGC TAT GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
1E2: -----

VH 3-33: GCA GTT ATA TGG TAT GAT GGA AGT AAT AAA TAC TAT GCA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC AGA
1E2: -----

CDR2

VH 3-33: GCA GTT ATA TGG TAT GAT GGA AGT AAT AAA TAC TAT GCA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC AGA
1E2: -----

FIG. 6
1 of 2



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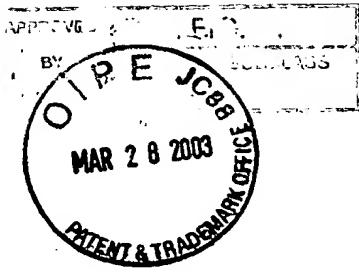
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VH 3-33 : GCG AGA GA
 1E2 : --- --- -CT CCC AAT TAT GGT GCT TTT GAT GTC TGG GGC CAA CGG ACA ATG GTC ACC GTC TCT TCA G/
 CDR3 _____
 J_H 3b _____

FIG. 6
2 of 2



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SEQ ID NOS : 5 , 7 & 9 (respectively)

	CDR1	CDR2	CDR3
VK A-27			
Germline:	EIVLTOSPGTLSLSPGERATLSC	RASQSVSSSYLA	WYQQKPGOAPRLLY
10D1:	-----	G-----	-----
4B6:	-----	-----	F-----

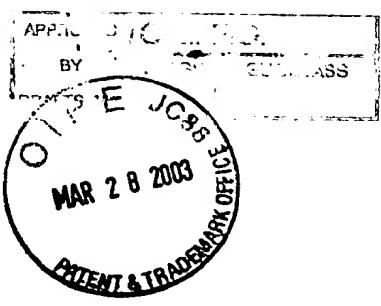
	CDR1	CDR2	CDR3
VK A-27 :	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGS	
10D1 :	-----	-----	PWT
4B6 :	-----	-----	FGQQGTVKEIK

SEQ ID NOS : 11 & 13 (respectively)

	CDR1	CDR2	CDR3
VK L-15			
Germline:	DIQMTQSPSSLSASVGDRVTITC	RASQGIGSSWLA	WYQQKPEKAFKSLIY
1E2:	-----	-----	-----

	CDR1	CDR2	CDR3
VK L-15 :	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	QQYNSY	
1E2 :	-----	-----	PPT
			FGQQGTVKEIK

FIG. 7



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SEQ ID NOS : 15, 17&19 (respectively)

		<u>CDR1</u>		<u>CDR2</u>	
VH 3-30.3		SYAMH	WVRQAPGKGLEWVA	VISYDGSNKKYYADSVKG	
Germline:	QVQLVESGGVVQPGRSRLSCAASGFTFS	-T--	-T-----	F-----N-----	
10D1:	-	-T--	-T-----	F-----T-----	
4B6:	-	-	-	H-----	

CDR3

VH 3-30.3 :	RFTISRDNSKNTLYLQMNSLRAEDTAVYCAR	
10D1:	-	I-----
4B6:	-	V-----
		TGWLGPFDY
		WGQGTLVTVSS

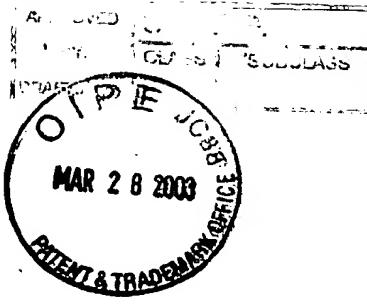
SEQ ID NOS : 21&23 (respectively)

		<u>CDR1</u>		<u>CDR2</u>	
VH 3-33		SYGMH	WVRQAPGKGLEWVA	VISYDGSNKKYYADSVKG	
Germline:	QVQLVESGGVVQPGRSRLSCAASGFTFS	-	-	-	
1E2:	-	-	-	-	

CDR3

VH 3-33 :	RFTISRDNSKNTLYLQMNSLRAEDTAVYCAR	
1E2:	-	-F-----
		APNYIGAFDV
		WGQGTMWTVSS

FIG. 8



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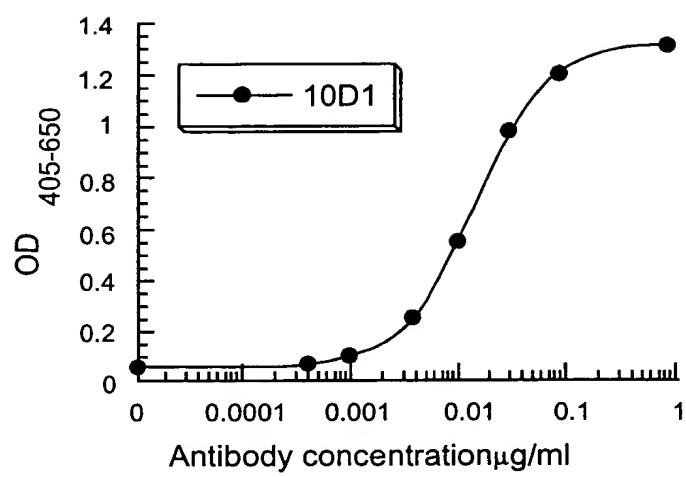
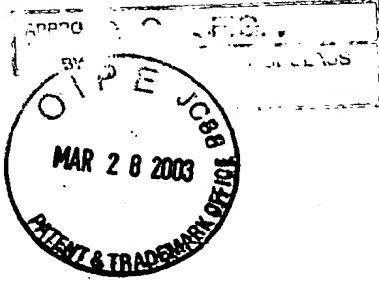


FIG. 9



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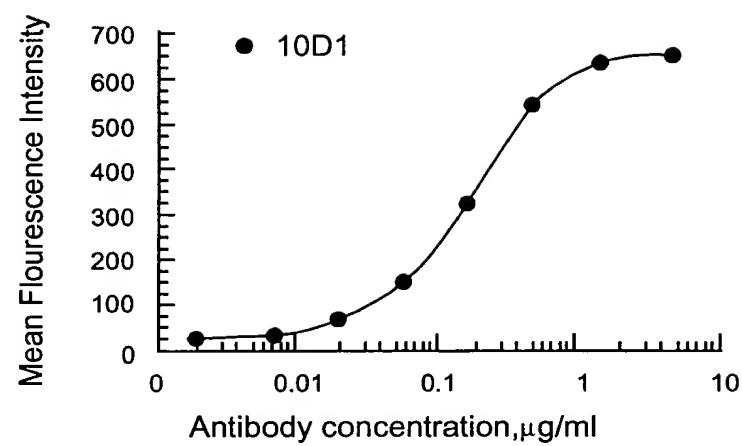
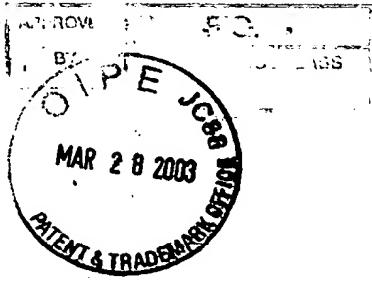


FIG. 10



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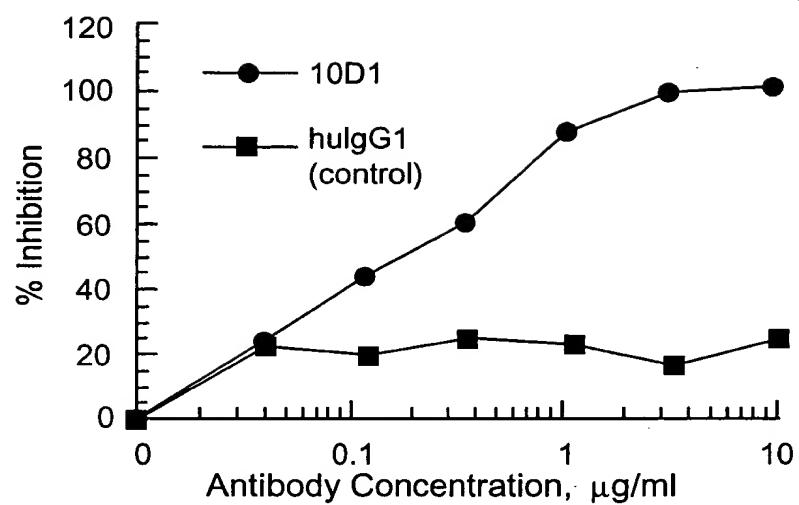
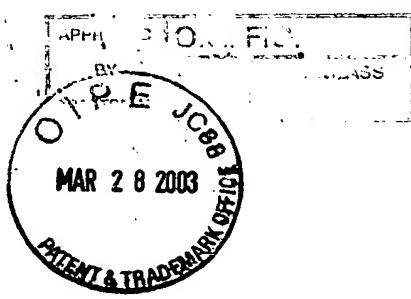


FIG. 11



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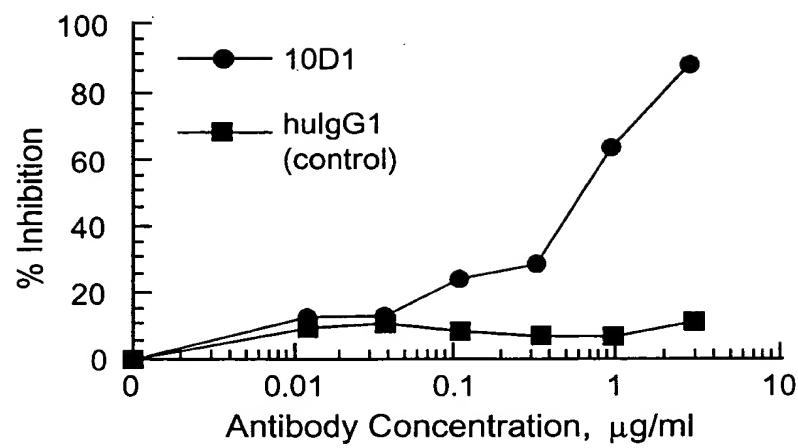


FIG. 12

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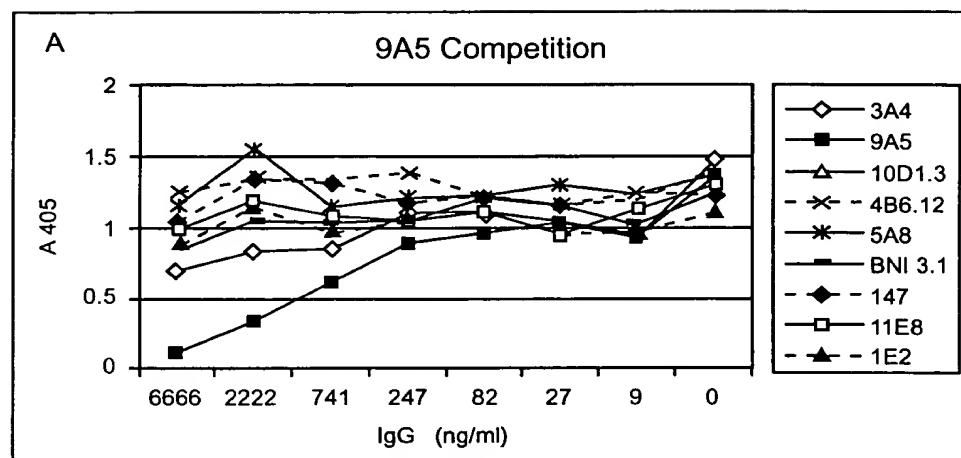


FIG. 13A

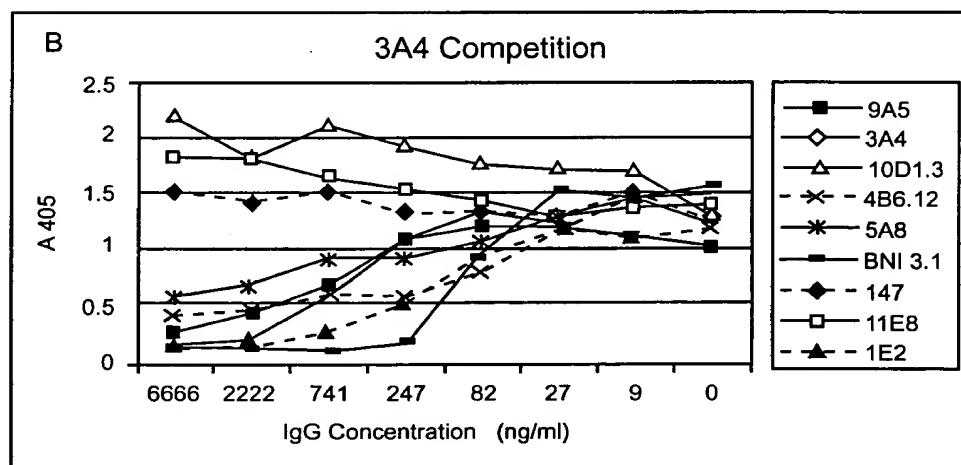


FIG. 13B

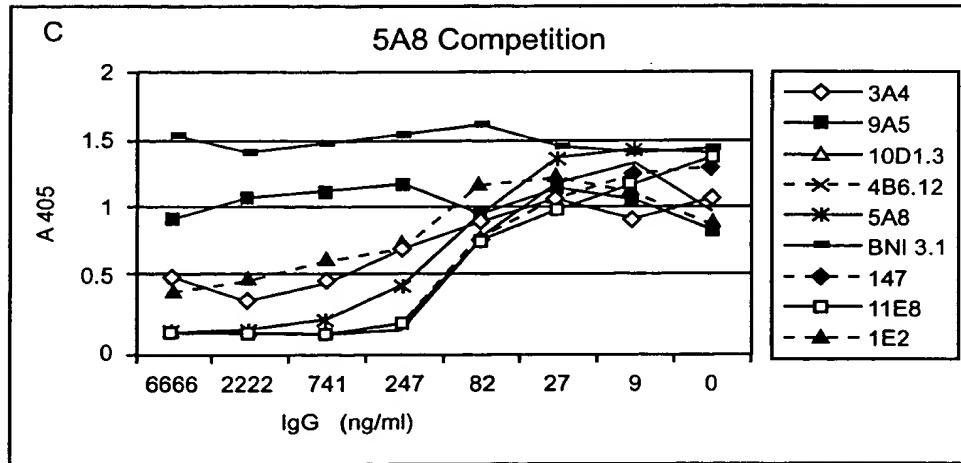


FIG. 13C



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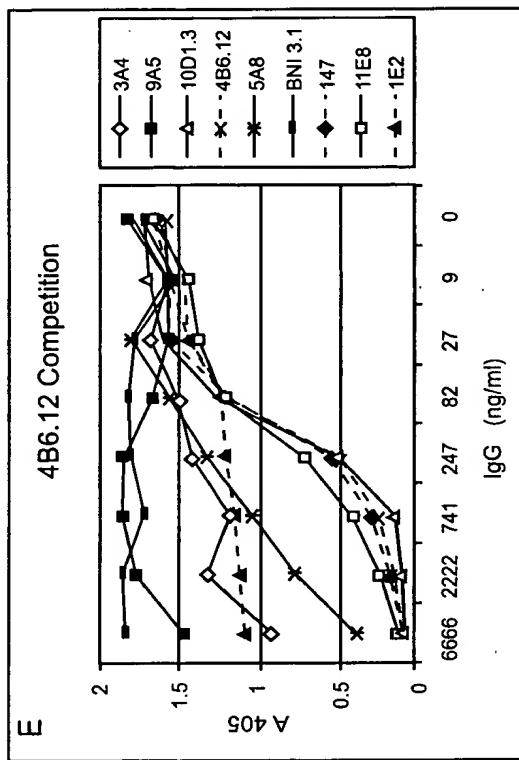


FIG. 13E

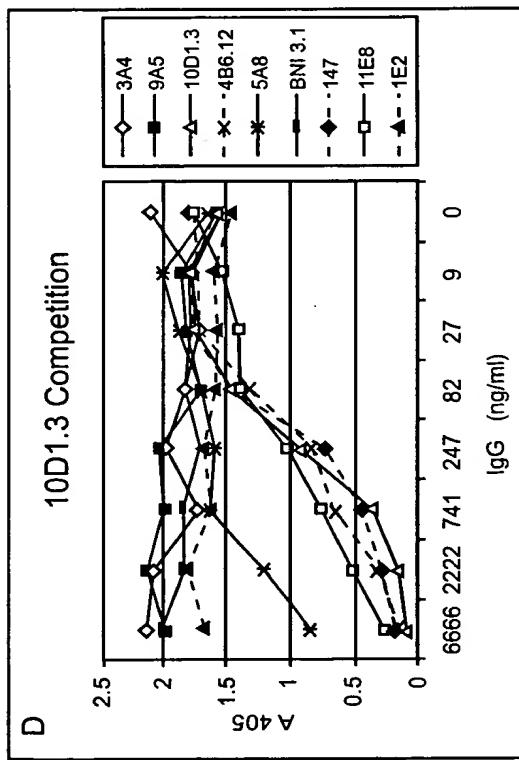


FIG. 13D

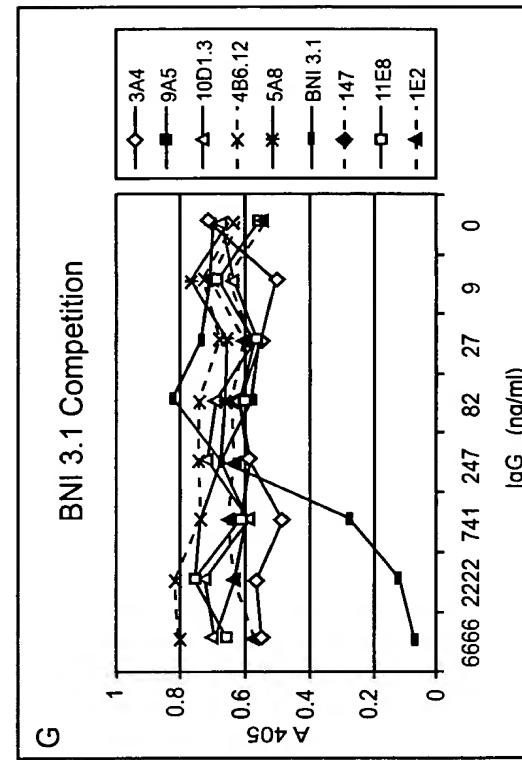


FIG. 13G

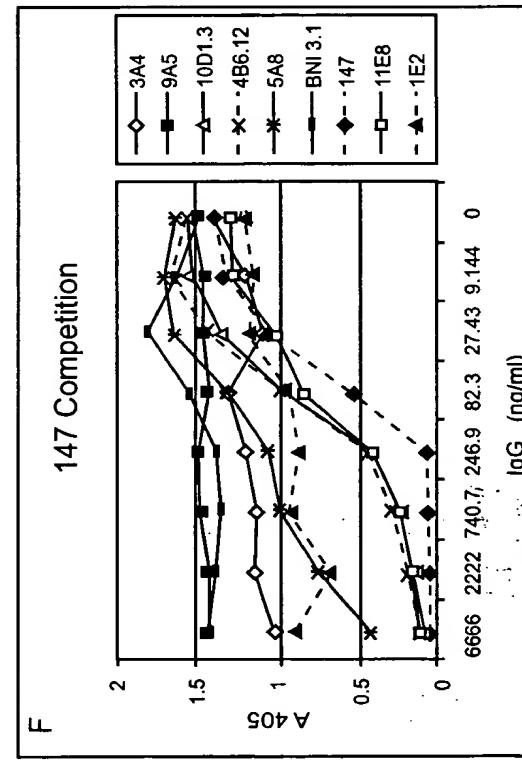


FIG. 13F

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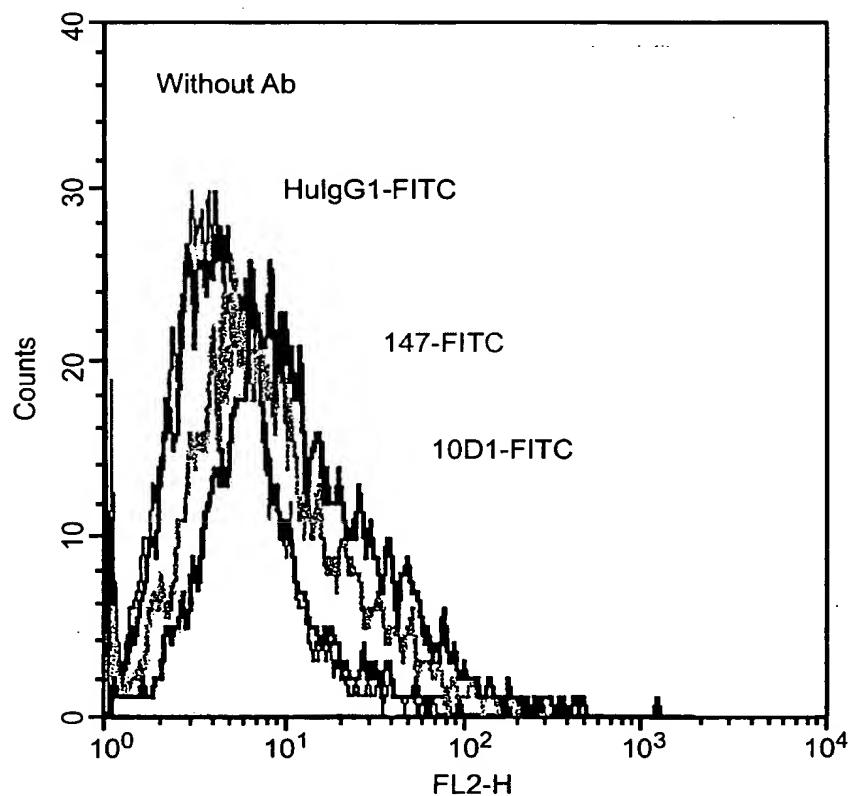
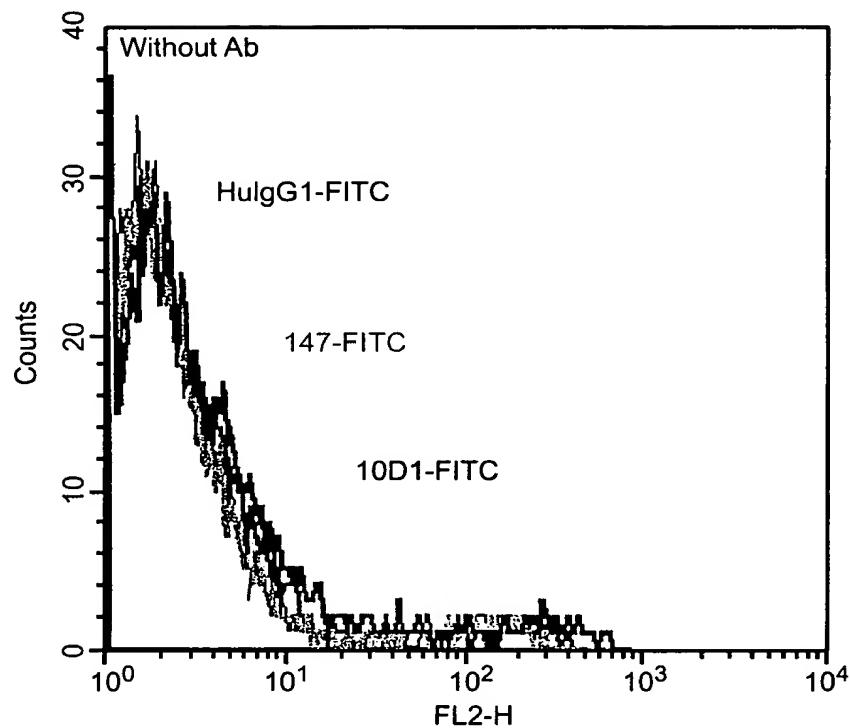
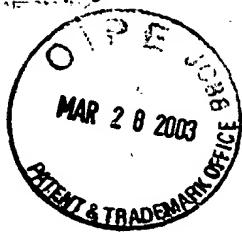


FIG. 14

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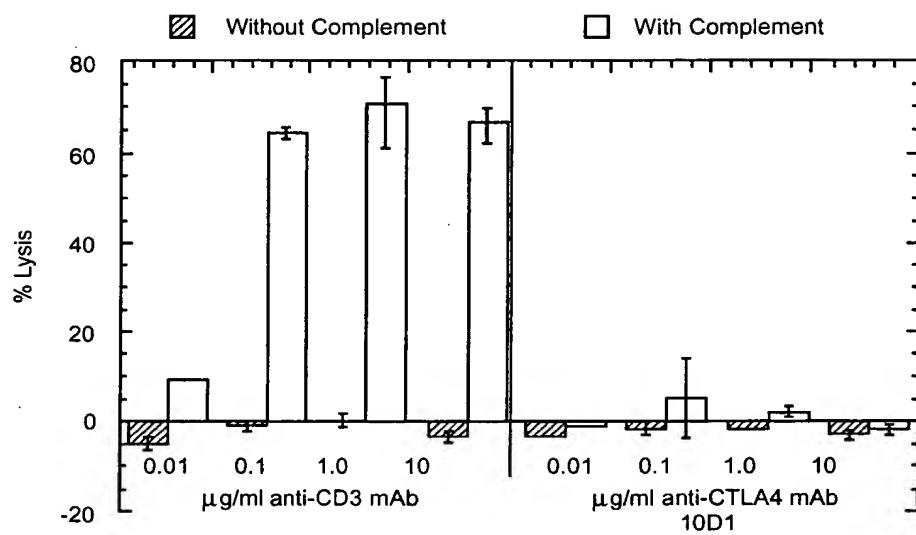


FIG. 15



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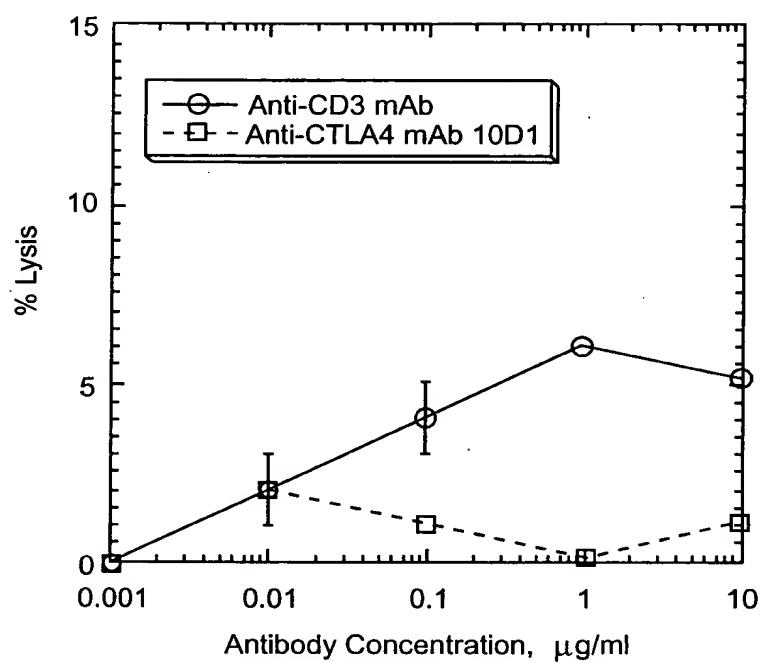


FIG. 16

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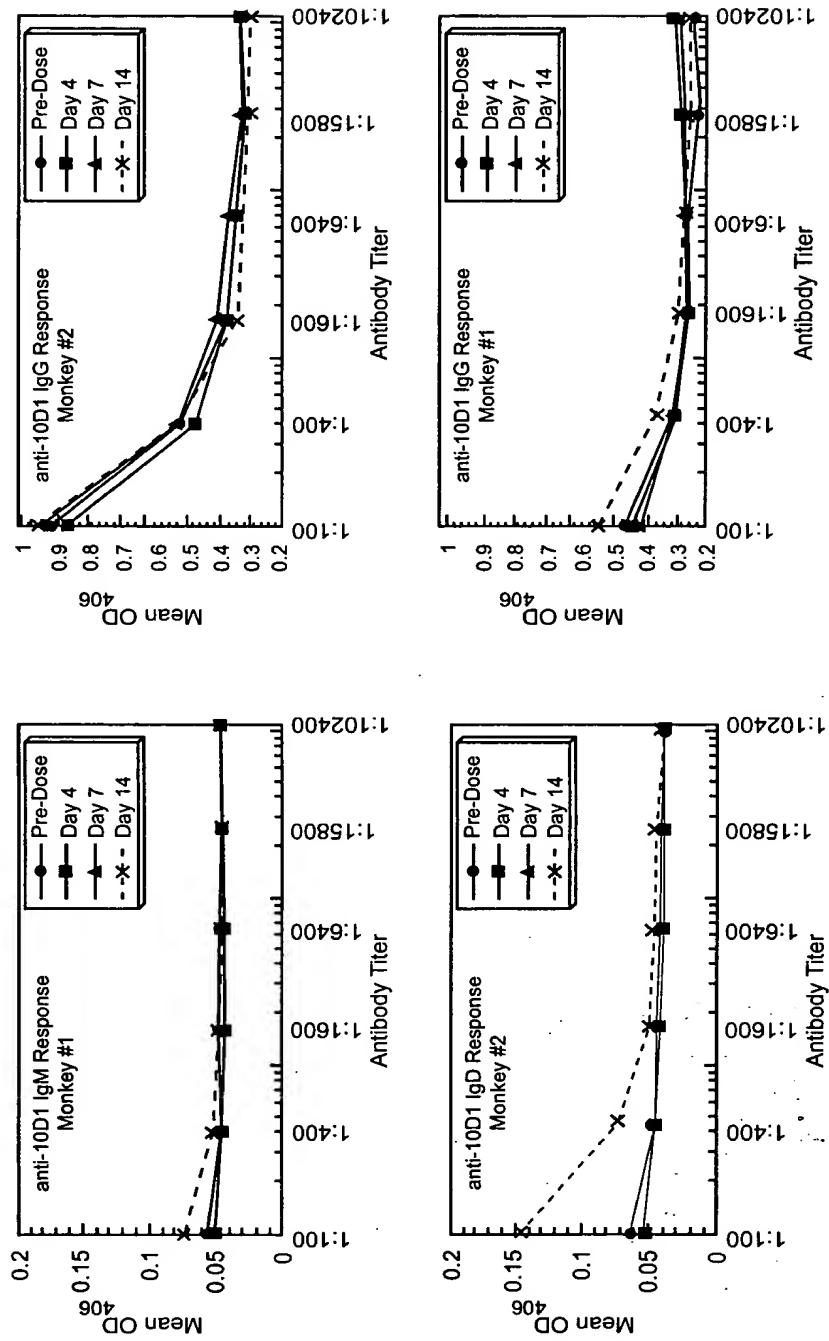


FIG. 17



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Study No. MDXGTLA4-01
Selected Lab Values Summary

Screen no.	Subject no.	Initials	Amendment #	Day	Date	PSA	Platelets	WBC	Neut	Lymph	Monos	Eos	Cd4	Cd8	ESR	Hgb	Hcrit			
						ng/ml	x10 ³ /ul	%	x10 ³ /ul	%	x10 ³ /ul	%	x10 ³ /ul	/ul	/ul	mmol/l	g/dl			
02001	001	JGR		Scr		144.80	263	8.12	73.00	5.90	18.00	1.47	5.60	0.46	1.80	0.15	10.4	30		
02001	001	JGR	0		185.20	287	5.74	66.00	3.79	22.00	1.32	6.60	0.38	3.10	0.18	67.0	367	71		
02001	001	JGR	1		259	6.31	69.00	4.38	20.00	1.29	8.70	0.55	0.90	0.00	A	A	9.5	30		
02001	001	JGR	2		240	6.59	70.00	4.66	19.00	1.31	6.70	0.44	1.80	0.12	556	303	9.5	28		
02001	001	JGR	3		270	6.53	71.00	4.63	21.00	1.36	5.50	0.36	2.20	0.14	608	254	9.3	28		
02001	001	JGR	7		257.40	299	6.70	68.00	4.56	23.00	1.53	6.00	0.40	2.50	0.17	A	A	9.5	28	
02001	001	JGR	14		332.30	308	6.87	71.90	7.94	21.20	1.39	5.21	0.36	1.90	0.13	A	A	8.8	25	
02001	001	JGR	21		286	9.72	74.00	7.20	19.70	1.91	4.80	0.46	1.00	0.10	A	A	9.1	28		
02001	001	JGR	28		351.00	304	5.38	63.00	3.40	26.00	1.44	5.80	0.31	2.90	0.16			8.7	25	
01002		JWF		Scr	28.30	271	11.60	75.40	8.75	13.60	1.58	5.70	0.56	4.60	0.53	399	189	41	13.9	37
01003		MZB		Scr	12.70	178	5.49	69.00	3.79	19.60	1.08	6.30	0.35	2.70	0.24	325	168	19	12.7	36
01004		TEQ		Scr	1459.00	264	6.26	75.10	4.70	14.40	0.90	7.70	0.48	2.40	0.15	365	129	61	12.8	36
01005		WMN		Scr	192.40	212	6.85	73.70	5.05	17.40	1.20	6.20	0.43	2.20	0.15	483	217			
01006		MRS		Scr	4503.00	140	7.55	76.70	5.79	15.90	1.20	6.20	0.47	0.80	0.06	319	363	83		
01007		TAB		Scr	1394.30	205	5.78	73.00	4.24	13.00	0.76	6.50	0.37	6.00	0.35	376	127		14.1	43
01008		CHB		Scr	70.70	229	4.67	54.00	2.56	32.00	1.52	8.30	0.38	3.40	0.16	461	499		15.6	45
01009	003	RAB		Scr	238.60	144	3.70	78.00	2.88	14.00	0.55	5.40	0.20	1.20	0.04	211	162	43	9.8	30
01009	003	RAB	0		336.90	123	3.92	68.00	2.67	21.00	0.83	8.70	0.34	1.50	0.06	374	188		10.9	31
01009	003	RAB	1		122	3.35	71.00	2.38	22.00	0.74	4.00	0.14	1.80	0.06	307	192		11.3	32	
01009	003	RAB	2		109	4.05	74.00	2.99	19.00	0.77	4.80	0.20	1.20	0.05	328	220		11.3	33	
01009	003	RAB	3		114	3.79	70.00	2.67	21.00	0.81	6.20	0.23	1.30	0.05	313	265		10.9	31	
01009	003	RAB	7		249.30	69	3.38	75.00	2.54	17.00	0.60	5.60	0.19	0.70	0.02	244	161		10.4	30
01009	003	RAB	14		269.80	101	3.68	69.00	2.54	21.20	0.78	8.50	0.31	1.00	0.04	308	173		8.8	25
01009	003	RAB	21		122	4.82	78.00	3.76	13.20	0.64	7.00	0.37	0.60	0.03	218	195		7.4	20	
01012	004	CEH		Scr	112.90	172	5.85	64.00	3.74	28.00	1.69	5.60	0.33	1.00	0.06	746	451	10	13.2	40
01012	004	CEH	1												642	475				
01012	004	CEH	2		150	4.82	67.70	3.26	26.40	1.28	4.60	0.22	1.10	0.05	552	380		12.2	36	
01012	004	CEH	3		147	4.36	63.70	2.78	29.30	1.28	5.10	0.22	1.30	0.06	544	441		13.1	37	
01012	004	CEH	7		190.00	159	4.95	58.60	2.90	32.70	1.61	5.90	0.29	2.50	0.12	842	506		12.6	35
01012	004	CEH	14		207.60	199	5.64	63.10	3.55	29.30	1.65	5.70	0.32	1.60	0.09			13.5	38	
01013		KJF		Scr	49.10	228	8.53	65.00	5.62	26.00	2.23	5.30	0.46	2.30	0.20	1213	398		13.4	37
02014	002	L-S		Scr	12.70	222	5.65	53.00	3.01	34.00	1.92	7.40	0.42	3.90	0.22	721	439		13.6	40
02014	002	L-S	0		27.50	217	5.88	57.00	3.36	32.00	1.88	8.60	0.50	1.50	0.09	676	389		13.5	38
02014	002	L-S	1		226	5.74	55.00	3.19	35.00	2.04	7.00	0.40	1.40	0.08	632	405		13.6	38	
02014	002	L-S	2		223	5.59	55.00	3.09	32.00	1.84	9.80	0.55	1.40	0.08	590	339		13.5	39	
02014	002	L-S	3		219	4.89	54.00	2.66	34.00	1.68	7.50	0.37	2.70	0.13	529	358		13.2	37	
02014	002	G-F		Scr	4856.00	106	7.31	86.00	6.29	5.00	0.33	6.80	0.49	1.90	0.14	57.6	7	10.3	31	
01016	Ineligible			normal range	150	3.80	40.50	1.96	15.40	0.80	2.60	0.12	4.04	0.20						
				high	7.00		10.70	75.00	7.23	48.50	3.00	10.00	0.92	6.80	0.57	1612	1128	30		

TABLE 11



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Study No. MDXCTLA4-02 Selected Lab Values Summary																			
Screen no.	Subject no.	Initials	Amendment #	Day	Date	Platelets $\times 10^3/\mu\text{l}$	WBC $\times 10^3/\mu\text{l}$	Neut	Lymph	Monos	Eos $\times 10^3/\mu\text{l}$	CD4	CD8	Hgb μl	Hcrit %				
02001	001	SAH	0	Scr		216	6.28	56.60	3.52	35.60	2.23	5.90	0.37	1.80	0.11	1189	631	14.4	39
02001	001	SAH	0	0		230	5.58	59.70	3.33	32.30	1.80	5.70	0.32	1.80	0.10	1039	502	14.9	43
02001	001	SAH	0	1		202	5.12	61.80	3.16	30.20	1.55	5.00	0.26	2.30	0.12	957	407	13.4	37
				normal range		150	3.80	40.50	1.96	15.40	0.80	2.60	0.12	1.10	0.04	220	1129	30	
				low		100	1.00	10.00	0.50	1.00	0.50	0.50	0.05	0.02	0.01	1612	1129	30	
				high		10.70	75.00	7.23	48.50	3.00	10.10	0.92	6.80	0.57	1612	1129	30		

TABLE 13